

Sequence Comparison A

RESULT 1

AAW18226

ID AAW18226 standard; Protein; 1495 AA.

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AC AAW18226;

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DT 24-SEP-1997 (first entry)

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DE Transcriptional co-repressor SMRT.

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KW Silencing mediator for retinoic acid and thyroid hormone receptor;

KW SMRT; transcriptional co-repressor.

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OS Homo sapiens.

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FH Key Location/Qualifiers

FT Region 1..160

FT /label= N-terminal_region

FT /note= "proline-rich domain"

FT Region 773..790

FT /label= ERDR_region

FT Region 812..827

FT /label= SG_region

FT Region 1061..1132

FT /label= glutamine-rich region

FT Region 1201..1495

FT /label= C-terminal_region

FT Peptide 1330..1376

FT /note= "alternatively spliced insert not
present in the original two-hybrid
clone"

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PN W09709418-A1.

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PD 13-MAR-1997.

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PF 24-JUL-1996; 96WO-US12371.

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PR 01-SEP-1995; 95US-0522726.

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PA (SALK) SALK INST BIOLOGICAL STUDIES.

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PI Chen JD, Evans RM;

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DR WPI; 1997-192894/17.

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PT New co-suppressor of steroid-thyroid hormone receptor activity -
PT also methods for identifying compounds that relieve its suppressant
PT effect and/or activate receptors

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PS Claim 2; Page 40-45; 71pp; English.

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CC A novel receptor interacting factor (AAW18226) is designated SMRT,
CC i.e. silencing mediator (co-repressor) for retinoic acid receptor
CC (RAR) and thyroid hormone receptor (TR). Its association with RAR
CC and TR both in solution and on DNA response elements is
CC destabilised by ligand. The interaction of SMRT with mutant
CC receptors correlates with the transcriptional silencing activities
CC of receptors. In vivo, SMRT functions as a potent co-repressor. A
CC GAL4 DNA binding domain fusion of SMRT behaves as a frank repressor
CC of a GAL4-dependent reporter. These data identify a novel class of
CC cofactor which is believed to represent an important mediator of
CC hormone action. Full-length cDNA for SMRT has been isolated from
CC a HeLa library in a two-hybrid screen using a GAL4 DNA binding
CC domain/RXR fusion protein as bait.

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SQ Sequence 1495 AA;

Query Match 57.5%; Score 1441; DB 18; Length 1495;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1024	AFAAAEQKLPGDPPCWTSGLPFPVPPREVIKASPHADPSAFSYAPPGHPLPLGLHDTAR	1083
Db	12	AFAAAEQKLPGDPPCWTSGLPFPVPPREVIKASPHADPSAFSYAPPGHPLPLGLHDTAR	71
Qy	1084	PVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMVQLHVPYSEHAKAPVGPVTMGLP	1143
Db	72	PVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMVQLHVPYSEHAKAPVGPVTMGLP	131
Qy	1144	LPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTALGSVPGGSITKGIP	1203
Db	132	LPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTALGSVPGGSITKGIP	191
Qy	1204	STRVPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSRDLRGREDSLPKGHVIYEGK	1263
Db	192	STRVPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSRDLRGREDSLPKGHVIYEGK	251
Qy	1264	KGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMEGRVGRAISSASIEGLMGR	1323
Db	252	KGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMEGRVGRAISSASIEGLMGR	311
Qy	1324	AIPPERHSPHHLKEQHHRGSITQGI PRSYVEAQEDYL RREAKLLKREGTPPPPPSRDL	1383
Db	312	AIPPERHSPHHLKEQHHRGSITQGI PRSYVEAQEDYL RREAKLLKREGTPPPPPSRDL	371
Qy	1384	TEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQ	1443
Db	372	TEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQ	431
Qy	1444	GTPLKYDTGASTTGSKKH D VRS LIGSPGR TFPVHPLDVMADARALERACYEESLSRPG	1503
Db	432	GTPLKYDTGASTTGSKKH D VRS LIGSPGR TFPVHPLDVMADARALERACYEESLSRPG	491
Qy	1504	TASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGS	1563
Db	492	TASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGS	551
Qy	1564	LSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLRGVSGVDLYRSHIPLAFD	1623
Db	552	LSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLRGVSGVDLYRSHIPLAFD	611
Qy	1624	PTSIPRGIPLDAAAAYLPRHLAPNPTYPHLYPPYLIRGYPDAALENRQTIINDYITSQ	1683
Db	612	PTSIPRGIPLDAAAAYLPRHLAPNPTYPHLYPPYLIRGYPDAALENRQTIINDYITSQ	671
Qy	1684	QMHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPAT	1743
Db	672	QMHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPAT	731
Qy	1744	AMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLT KPTTTSSSERERDRDRERDREREKS	1803
Db	732	AMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLT KPTTTSSSERERDRDRERDREREKS	791
Qy	1804	ILTSTTTVEHAPIWRPGTEQSSGSSGSSGGGGSSSRPASHSHAHQHSPISPRTDALQQ	1863
Db	792	ILTSTTTVEHAPIWRPGTEQSSGSSGSSGGGGSSSRPASHSHAHQHSPISPRTDALQQ	851
Qy	1864	RPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVYPTLM	1923
Db	852	RPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVYPTLM	911
Qy	1924	EPVLLPKEAPRVARPERPRADTGHAF LAKPPARSGLEPASSPSKGSEPRPLVPPVSGHAT	1983
Db	912	EPVLLPKEAPRVARPERPRADTGHAF LAKPPARSGLEPASSPSKGSEPRPLVPPVSGHAT	971
Qy	1984	IARTPAKNLAPHHASPDPPAPPASADPHREKTQSKPFSIQELELRLSLGYHGSSYSPEGV	2043
Db	972	IARTPAKNLAPHHASPDPPAPPASADPHREKTQSKPFSIQELELRLSLGYHGSSYSPEGV	1031

Qy	2044	EPVSPVSSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQ	2103
Db	1032	EPVSPVSSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQ	1091
Qy	2104	PSSSPLLQTAPGVKGHRVVTLAQHISEVITQDYTRHHPQQLSAPLPAPLYSFPGASCPV	2163
Db	1092	PSSSPLLQTAPGVKGHRVVTLAQHISEVITQDYTRHHPQQLSAPLPAPLYSFPGASCPV	1151
Qy	2164	LDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVSPPGEMTE	2223
Db	1152	LDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVSPPGEMTE	1211
Qy	2224	PGHSRSVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSAMVSKKQEINKK	2283
Db	1212	PGHSRSVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKLTESNSAMVSKKQEINKK	1271
Qy	2284	LNTHNRNEPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGK	2343
Db	1272	LNTHNRNEPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGK	1331
Qy	2344	YDQWEESPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGGGKAKVSGRPSSRK	2403
Db	1332	YDQWEESPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGGGKAKVSGRPSSRK	1391
Qy	2404	AKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPPFPYNPLIMRLQA	2463
Db	1392	AKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPPFPYNPLIMRLQA	1451
Qy	2464	G	2464
Db	1452	G	1452